Week 9: Phylogeny, paleontology, and practical applications

Phylogenetic software

For this lab you will need to download and install the Mesquite, PHYLIP, and Phylogenetics for Mathematica packages:

http://mesquiteproject.org/mesquite/mesquite.html
http://evolution.genetics.washington.edu/phylip.html
http://mypage.iu.edu/~pdpolly/Software.html

Mesquite. Mesquite has tools for creating and modifying phylogenetic data matrices, as well as tools for displaying trees and doing certain kinds of analysis on phylogenetic data. It does not, however, do an exhaustive parsimony analysis. Mesquite's documentation can be found by opening the file "documentation.html" in your web browser.

PHYLIP. PHYLIP (Phylogenetic Inference Package) has modules for estimating phylogenetic trees from data and for displaying the trees. We will use the *Pars* module, which calculates a parsimony tree from multistate data, and the *Consense* module, which calculates a consensus tree (average) when more than one tree is found by *Pars*. We will also use the *ContML* module, which calculates a maximum likelihood tree from continuous data. PHYLIP's documentation can be found in the folder "docs" where you stored the PHYLIP package on your computer.

Phylogenetics for Mathematica. An add-in package for Mathematica that performs several simple tree-related tasks, such as reading in a Newick format tree file, drawing trees, rerooting them, simulating data on the trees, reconstructing ancestral nodes from the trees, and doing independent contrasts. It also helps prepare data for export to PHYLIP. For this course, we will only use the tree reading and drawing functions.

Running PHYLIP

Documentation. read the following pages in the PHYLIP documentation. Start by opening the help file Main.html into your web browswer. Read it, then read the following:

discrete characters
Pars
Penny
Consense

I've uploaded two example data files to the website. One is made of up discrete characters from selected credonts (mammalian carnivores from the Paleogene) from Polly (1996). (the dataset on

Oncourse is not identical to the one in the paper; some errors have been corrected, including removal of a redundant character). The other is made up of quantitative traits describing the shape of molars in marmots (big ground squirrels from the Neogene) from Polly (2003). You can use these to get used to the program.

Polly, P. D. 1996 The skeleton of Gazinocyon vulpeculus gen et comb nov and the cladistic relationships of Hyaenodontidae (Eutheria, Mammalia). *Journal of Vertebrate Paleontology* **16**, 303-319.

Polly, P. D. 2003 Paleophylogeography: The tempo of geographic differentiation in marmots (Marmota). *Journal of Mammalogy* **84**, 369-384.

Both files are in the PHYLIP format, which is described in Felsenstein's documentation. Basically the format consists of a first line with two numbers, number of taxa and number of characters, followed by lines that begin with a short taxon name followed by the character data.

The easiest way to run PHYLIP is to save the file you are working with in the folder with the PHYLIP programs. Name the file "infile". Note that Windows often adds an extension (such as .txt) that may be hidden depending on your folder settings. PHYLIP saves output data in the files OUTFILE and OUTTREE. The latter can be renamed with a ".tre" extension and opened in TreeView.

Parsimony Analysis

The PARS and PENNY programs do parsimony analysis. PARS handles characters with more states than just 0 and 1. PENNY is more efficient than PARS for some data sets.

To run a parsimony analysis on the data in the file "INFILE" double click on PARS to start the program. You are first faced with several options: type the letter in the left column to change the associated option. You probably want to change the J option to randomize the input order (the search sometimes is influenced by input order), you might also want to change option O (outgroup). For the creodont data, set the outgroup to taxon 1 (which is a dummy outgroup taxon coded with all ancestral character states).

Note that characters are considered to be *unordered* in PARS, which means that only one tree step is required for a character to change from 0 to 1, 0 to 2, 0 to 3, 1 to 3, etc. This makes sense in many cases if you don't know the order of transition, but in other cases it may not make sense (e.g., digit reduction might reasonably be assumed to go from 5 to 4 to 3 to 2 to 1 and not jump straight from 5 to 1).

When you are satisfied with your options, type Y to start the analysis. Progress reports will be printed on the screen. When the program is finished, open OUTFILE in a text editor to see the results. The creodont dataset yields 12 equally parsimonious trees, each with 114 steps.

The OUTTREE file can be viewed in Mesquite (it's easiest to change the extension to .tre first and you **MUST** remove the carriage returns from within each tree so that each one is on a separate line **AND** remove the last number before the semicolon and its two square brackets). Open the file and choose "Phylip (trees)" as the type when prompted to do so. You can see all 12 trees in Mesquite by clicking on the View Trees icon and then paging through the trees with the arrow button at the top of the screen. The first tree looks like this:

You can also view trees one at a time in Mathematica. Load the Phylogenetics package:

```
<<PollyPhylogenetics`
```

Then copy and paste the tree of interest into a file of its own. For example:

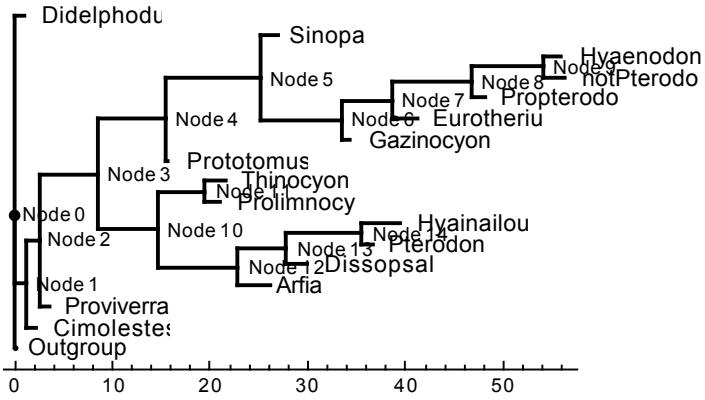
(Didelphodu:1.00,(((((Sinopa:1.79,((((Hyaenodon:1.87,notPterodo:2.20):7.24,Propterodo:1.23):8.14,Eurotheriu:2.47):5.22,Gazinocyon:0.88):8.25):9.85,Prototomus:0.36):6.80,((Thinocyon:2.10,Prolimnocy:1.67):4.78,(((Hyainailou:4.00,Pterodon:1.25):7.67,Dissopsali:2.17):4.93,Arfia:3.19):8.26):6.05):6.08,Proviverra:1.00):1.29,Cimolestes:1.00):1.29,Outgroup:0.00);

Then read in the tree:

```
tree = ReadNewick['tree1.tre'];
```

And plot the tree:

```
DrawNewickTree[tree]
```



Consensus trees

You can collapse twelve trees into a "consensus" tree using the CONSENSE program in PHYLIP. Rename your OUTTREE file as "INTREE" and double-click CONSENSE (if you don't rename, you can specify the input file when the program starts). You can specify the type of consensus as Majority Rule (this option retains the nodes that are found in a majority of trees) or Strict (which only retains nodes found in all trees). A large literature exists on these consensus methods.

You can choose to specify an outgroup (which should be taxon 1 for this data set) and to treat the trees as rooted (which is appropriate for this data set). The strict consensus tree from the creodont data set looks like the following. (note that this doesn't look like the tree published in Polly, 1996 because of the corrected error and because that analysis used ordered character transformations for several multi-state characters).

In Mesquite the strict consensus tree looks like the following. (you must again remove the carriage returns from the file). Note that you can't load this tree into Mathematica because Consensus trees don't have branch lengths and the ReadNewick[] function requires them.

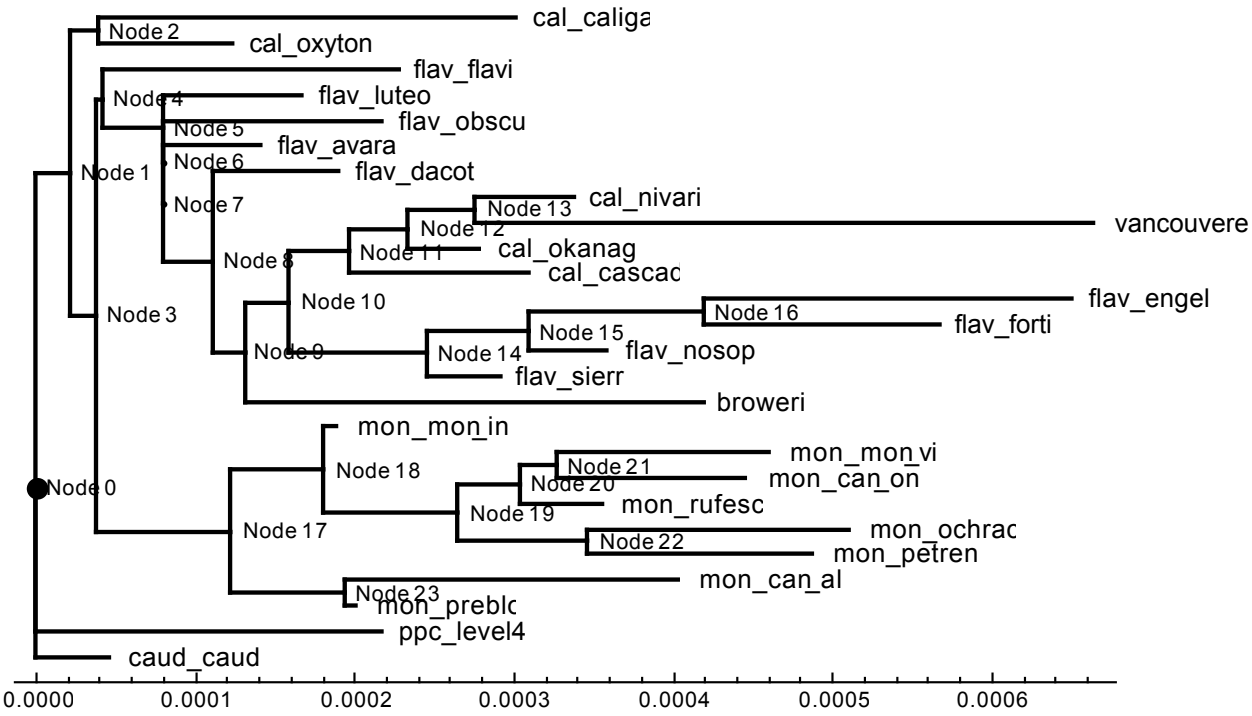
The OUTFILE contains a text representation of the trees and other useful information, including the number of steps in the trees and the number of character changes along each branch. Depending on the options you chose, you may also find descriptions of where the characters change on the tree, etc. Unfortunately, PARS does not calculate consistency index (CI). To calculate this, divide the total number of character changes in your data matrix by the length of the tree. If your characters are all single state (i.e., 0 and 1) then the total number of changes is simply the number of characters. If you have multistate characters, then it is the sum of all non-zero states across all the characters. In the creodont data set there are 78 possible character changes, which gives CI = 0.68 for the 12 trees found here.

Quantitative Traits with CONTML

CONTML does a maximum likelihood analysis on quantitative traits. The example data set from Polly (2003) is based on geometric morphometric shape, but data can be of any type (e.g., length and width measurements). Like with PARS, the data should be in PHYLIP format and saved in the file "INFILE" in the same folder as the program.

Double-click CONTML to start. Use the C option to select "continuous characters", the J option to randomize the input order, and any other options you like. Type Y to start the analysis. Look in OUTFILE for the output of the run and in OUTTREE for the trees produced (change extension to ".tre" and remove carriage returns to view in Mesquite).

The tree found from the marmot data set has a log likelihood of 2449.45 and looks like the following. Note that the log likelihood is nearly meaningless for comparing with other data sets, but could be useful for deciding how much better supported the best tree is compared to others for the same data set.



Bayesian Analysis with Mr Bayes

Mr Bayes is phylogenetic analysis software for conducting Bayesian searches of tree space. The software is written by Ronquist and Huelsenback and can be obatained at: http://mrbayes.csit.fsu.edu/

Data should be formatted in NEXUS format (http://hydrodictyon.eeb.uconn.edu/eebedia/index.php/Phylogenetics:_NEXUS_Format) and the installation package comes with several example files. For morphological data, the "Standard" data type is used.

The user manual gives a good, quick introduction to the program and to Bayesian analysis in general, though the text is geared toward molecular data. A good introduction to Bayesian analysis of morphological data in Mr Bayes can be had from University of Connecticut:

http://hydrodictyon.eeb.uconn.edu/eebedia/index.php/Phylogenetics:_Morphology_and_Partitioning_in_MrBayes

Assignment

1. Analyze the creodont data set with *Pars*. Show the second tree in the data set and the consensus tree.

2. Calculate the consistency index for the creodont tree.

3. Analyze the marmot data set with *Contml*. Show the tree and report the maximum likelihood.

4. Do the reading:

Reading for Next Week

Fisher, D. C. 2008 Stratocladistics: integrating temporal data and character data in phylogenetic inference. Annual Review of Ecology and Systematics 39, 365-385.

Gingerich, P. D. 1979 The stratophenetic approach to phylogeny reconstruction in vertebrate paleontology. In Phylogenetic Analysis and Paleontology (ed. J. Cracraft & N. Eldredge), pp. 41-77. New York: Columbia University Press.

Wagner, P. J. 1998. A likelihood approach for evaluating estimates of phylogenetic relationships among fossil taxa. *Paleobiology*, 24: 430-449.